PCT09

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/647,377   TIME: 15:05:38

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Output Set: N:\CRF3\11142001\I647377.raw

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 3 <110> APPLICANT: Rosenthal, Andre et al.
 5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING PROTEINS WHICH INFLUENCE
BONE DEVELOPMENT
 7 <130> FILE REFERENCE: 0147-0211P
 9 <140> CURRENT APPLICATION NUMBER: 09/647,377
C--> 10 <141> CURRENT FILING DATE: 2000-09-24
12 <160> NUMBER OF SEQ ID NOS: 34
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1550
18 <212> TYPE: DNA
19 <213> ORGANISM: Mus musculus
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (2)..(1180)
24 <223> OTHER INFORMATION:
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30    1              5                  10                  15
32 gtc cag aag gtg gtc ccc atg ctt ccc agg ctt ctg tgt gag gaa ctc      97
33 Val Gln Lys Val Val Pro Met Leu Pro Arg Leu Leu Cys Glu Glu Leu
34             20                  25                  30
36 tgc agc ctc aac ccc atg act gac aag ctg acc ttc tct gtg atc tgg     145
37 Cys Ser Leu Asn Pro Met Thr Asp Lys Leu Thr Phe Ser Val Ile Trp
38         35                  40                  45
40 aag ctg acc cct gaa ggc aag atc ctt gaa gag tgg ttt ggc cgc act     193
41 Lys Leu Thr Pro Glu Gly Lys Ile Leu Glu Glu Trp Phe Gly Arg Thr
42     50                  55                  60
44 atc atc cgt tct tgc acc aaa ctg agc tac gac cat gcc cag agc atg     241
45 Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Asp His Ala Gln Ser Met
46 65                  70                  75                  80
48 atc gaa aat cca act gag aag atc cct gag gaa gag ctt ccc cca att     289
49 Ile Glu Asn Pro Thr Glu Lys Ile Pro Glu Glu Glu Leu Pro Pro Ile
50                 85                  90                  95
52 tct cca gag cac agc gtc gag gag gtg cac cag gca gtc ctg aac ctg     337
53 Ser Pro Glu His Ser Val Glu Glu Val His Gln Ala Val Leu Asn Leu
54             100                 105                 110
56 cac agc att gca aag caa ctc cgc cgc cag cgc ttt gta gat ggc gca     385
57 His Ser Ile Ala Lys Gln Leu Arg Arg Gln Arg Phe Val Asp Gly Ala
58             115                 120                 125
60 ctc cgt tta gat cag gag ttc atg ctc ctg gcc aac atg gcg gtg gcc     433
61 Leu Arg Leu Asp Gln Glu Phe Met Leu Leu Ala Asn Met Ala Val Ala
62     130                 135                 140
64 cac aag atc ttc cgc acc ttc cct gag cag gcc ctg ctg cgc cgg cat     481
65 His Lys Ile Phe Arg Thr Phe Pro Glu Gln Ala Leu Leu Arg Arg His
66 145                 150                 155                 160
68 ccc cca cca cag acg aag atg ctc agt gac ctg gtg gag ttc tgt gac     529
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69  Pro Pro Pro Gln Thr Lys Met Leu Ser Asp Leu Val Glu Phe Cys Asp
70              165                 170                 175
72  cag atg ggg ctg ccc atg gat gtc agc tct gca ggg gcc cta aat atg     577
73  Gln Met Gly Leu Pro Met Asp Val Ser Ser Ala Gly Ala Leu Asn Met
74              180                 185                 190
76  gca ctg tac ttc tgc tct ggg atg ctg cag gac cag gag cag ttc cgg     625
77  Ala Leu Tyr Phe Cys Ser Gly Met Leu Gln Asp Gln Glu Gln Phe Arg
78              195                 200                 205
80  cat tat gct ctc aac gtt ccc ctc tac aca cac ttc acc tct ccc atc     673
81  His Tyr Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile
82      210                 215                 220
84  cgc cgc ttt gct gac gtc ata gtg cac cgc ctc ctg gct gct gct ctg     721
85  Arg Arg Phe Ala Asp Val Ile Val His Arg Leu Leu Ala Ala Ala Leu
86  225                 230                 235                 240
88  ggc tac agt gaa cag cca gat gtg gag cct gat acc cta cag aag caa     769
89  Gly Tyr Ser Glu Gln Pro Asp Val Glu Pro Asp Thr Leu Gln Lys Gln
90              245                 250                 255
92  gct gac cac tgc aat gac cgt cgc atg gct tcc aaa cgt gtg cag gag     817
93  Ala Asp His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu
94              260                 265                 270
96  ctc agc atc ggc ctc ttc ttc gca gtt cta gta aag gag agt ggc ccc     865
97  Leu Ser Ile Gly Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro
98          275                 280                 285
100 ctg gag tcc gaa gcc atg gtg atg ggt gtc ctg aac caa gct ttc gac     913
101 Leu Glu Ser Glu Ala Met Val Met Gly Val Leu Asn Gln Ala Phe Asp
102     290                 295                 300
104 gtg ctg gtg ctg cgc ttt ggg gtg cag aag cgc atc tac tgc aat gca     961
105 Val Leu Val Leu Arg Phe Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala
106 305                 310                 315                 320
108 ctg gcc ctg cga tcc tac agc ttc cag aag gtg ggg aag aag cca gag     1009
109 Leu Ala Leu Arg Ser Tyr Ser Phe Gln Lys Val Gly Lys Lys Pro Glu
110             325                 330                 335
112 ctc act ctt gtt tgg gag cct gat gac ctt gaa gag gag cca aca cag     1057
113 Leu Thr Leu Val Trp Glu Pro Asp Asp Leu Glu Glu Glu Pro Thr Gln
114             340                 345                 350
116 cag gtc atc acc atc ttc agc ctg gtg gat gtg gtc ctg cag gca gag     1105
117 Gln Val Ile Thr Ile Phe Ser Leu Val Asp Val Val Leu Gln Ala Glu
118             355                 360                 365
120 gcc aca gcc ctc aag tac agt gct atc ctg aag cga cca ggc ctg gag     1153
121 Ala Thr Ala Leu Lys Tyr Ser Ala Ile Leu Lys Arg Pro Gly Leu Glu
122     370                 375                 380
124 aag gcg tct gat gag gag cct gag gac tgaatgctag cccaagccag         1200
125 Lys Ala Ser Asp Glu Glu Pro Glu Asp
126 385                 390
128 gcctgtgcct gccctaccct gctggctttt aggaatagga ccttttgaca ccaaagggga    1260
130 tttttaattt ggttttttaac aactcagggg tttgtttttta tttttatttt tccttttatt   1320
132 ttacttttgc agctcagttt ttaaatgaac tggaaggtta ggggtcaggg caggggatgc     1380
134 tgaggcctgg cctgtgcttc cctgagcaga gaggatccca gtcctcctgg gcaggcagcc     1440
136 ccgcttctac caggcgaccc actgcccttc cctgcccagg aaatggggggg tttcagcaaa    1500
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142 <211> LENGTH: 393
143 <212> TYPE: PRT
144 <213> ORGANISM: Mus musculus
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152 Val Gln Lys Val Val Pro Met Leu Pro Arg Leu Leu Cys Glu Glu Leu
153             20                  25                  30
156 Cys Ser Leu Asn Pro Met Thr Asp Lys Leu Thr Phe Ser Val Ile Trp
157         35                  40                  45
160 Lys Leu Thr Pro Glu Gly Lys Ile Leu Glu Glu Trp Phe Gly Arg Thr
161     50                  55                  60
164 Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Asp His Ala Gln Ser Met
165 65                  70                  75                  80
168 Ile Glu Asn Pro Thr Glu Lys Ile Pro Glu Glu Glu Leu Pro Pro Ile
169                 85                  90                  95
172 Ser Pro Glu His Ser Val Glu Glu Val His Gln Ala Val Leu Asn Leu
173             100                 105                 110
176 His Ser Ile Ala Lys Gln Leu Arg Arg Gln Arg Phe Val Asp Gly Ala
177         115                 120                 125
180 Leu Arg Leu Asp Gln Glu Phe Met Leu Leu Ala Asn Met Ala Val Ala
181     130                 135                 140
184 His Lys Ile Phe Arg Thr Phe Pro Glu Gln Ala Leu Leu Arg Arg His
185 145                 150                 155                 160
188 Pro Pro Pro Gln Thr Lys Met Leu Ser Asp Leu Val Glu Phe Cys Asp
189                 165                 170                 175
192 Gln Met Gly Leu Pro Met Asp Val Ser Ser Ala Gly Ala Leu Asn Met
193             180                 185                 190
196 Ala Leu Tyr Phe Cys Ser Gly Met Leu Gln Asp Gln Glu Gln Phe Arg
197         195                 200                 205
200 His Tyr Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile
201         210                 215                 220
204 Arg Arg Phe Ala Asp Val Ile Val His Arg Leu Leu Ala Ala Ala Leu
205 225                 230                 235                 240
208 Gly Tyr Ser Glu Gln Pro Asp Val Glu Pro Asp Thr Leu Gln Lys Gln
209             245                 250                 255
212 Ala Asp His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu
213         260                 265                 270
216 Leu Ser Ile Gly Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro
217         275                 280                 285
220 Leu Glu Ser Glu Ala Met Val Met Gly Val Leu Asn Gln Ala Phe Asp
221     290                 295                 300
224 Val Leu Val Leu Arg Phe Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala
225 305                 310                 315                 320
228 Leu Ala Leu Arg Ser Tyr Ser Phe Gln Lys Val Gly Lys Lys Pro Glu
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232 Leu Thr Leu Val Trp Glu Pro Asp Asp Leu Glu Glu Glu Pro Thr Gln
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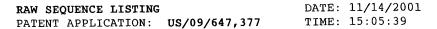
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PATENT APPLICATION: US/09/647,377   TIME: 15:05:39

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Output Set: N:\CRF3\11142001\I647377.raw

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233              340              345              350
236 Gln Val Ile Thr Ile Phe Ser Leu Val Asp Val Val Leu Gln Ala Glu
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244 Lys Ala Ser Asp Glu Glu Pro Glu Asp
245 385              390
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249 <211> LENGTH: 1140
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251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (2)..(781)
256 <223> OTHER INFORMATION:
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261   Ile His Arg Ala Phe Pro Glu Gln Ala Leu Leu Arg Arg His Pro Pro
262   1               5                10               15
264 ccc caa aca agg atg ctc agt gac ctg gtg gaa ttc tgc gac cag atg      97
265 Pro Gln Thr Arg Met Leu Ser Asp Leu Val Glu Phe Cys Asp Gln Met
266             20               25               30
268 ggg ctg ccc gtg gac ttc agc tcc gca gga gcc ctc aat atg gca ctg     145
269 Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn Met Ala Leu
270             35               40               45
272 tac ttc tgc tcg ggg ctg ctg cag gac cca gcg cag ttc cgg cac tac     193
273 Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr
274     50               55               60
276 gcg ctc aat gtg ccc ctg tac aca cac ttc acc tcg ccc atc cgc cgc     241
277 Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile Arg Arg
278 65               70               75               80
280 ttt gcc gac gtc ctg gtg cac cgc ctc ctg gct gcc gcg tta ggc tat     289
281 Phe Ala Asp Val Leu Val His Arg Leu Leu Ala Ala Ala Leu Gly Tyr
282             85               90               95
284 agg gag cga cta gac atg gcg ccc gat acc ctg cag aaa cag gcg gac     337
285 Arg Glu Arg Leu Asp Met Ala Pro Asp Thr Leu Gln Lys Gln Ala Asp
286             100              105              110
288 cac tgt aac gac cgc cgc atg gcg tcc aag cgc gtg cag gag ctc agt     385
289 His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu Leu Ser
290         115              120              125
292 acc agt ctc ttc ttt gct gtt ctg gtc aag gag agt ggc ccc ctg gag     433
293 Thr Ser Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro Leu Glu
294     130              135              140
296 tca gaa gcc atg gtg atg ggc atc ctg aag caa gcc ttc gac gtg ctg     481
297 Ser Glu Ala Met Val Met Gly Ile Leu Lys Gln Ala Phe Asp Val Leu
298 145              150              155              160
300 gtg ctg cgc tac ggc gtg cag aag cgc atc tac tgc aac gca ctg gcc     529
301 Val Leu Arg Tyr Gly Val Gln Lys Arg Ile Tyr Cys Asn Ala Leu Ala
302              165              170              175
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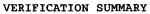
RAW SEQUENCE LISTING　　　　　DATE: 11/14/2001
PATENT APPLICATION: US/09/647,377　　TIME: 15:05:39

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\11142001\I647377.raw

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304 ctg cgg tcc cac cac ttc cag aag gtg ggc aag aag ccg gaa ctc acg    577
305 Leu Arg Ser His His Phe Gln Lys Val Gly Lys Lys Pro Glu Leu Thr
306             180                 185                 190
308 ctg gtc tgg gag cct gag gac atg gag cag gag cca gca cag cag gtc    625
309 Leu Val Trp Glu Pro Glu Asp Met Glu Gln Glu Pro Ala Gln Gln Val
310             195                 200                 205
312 atc acc atc ttc agc ctg gtg gag gtg gtc ctg cag gca gag tcc aca    673
313 Ile Thr Ile Phe Ser Leu Val Glu Val Val Leu Gln Ala Glu Ser Thr
314     210                 215                 220
316 gcc ctc aag tac agc gcc atc ctg aag cgg cca ggc acc cag ggc cac    721
317 Ala Leu Lys Tyr Ser Ala Ile Leu Lys Arg Pro Gly Thr Gln Gly His
318 225                     230                 235             240
320 ctg ggc cct gag aag gag gag gag gag tct gac ggt gag ccc gag gac    769
321 Leu Gly Pro Glu Lys Glu Glu Glu Glu Ser Asp Gly Glu Pro Glu Asp
322             245                 250                 255
324 tca agc acc agc tgagctccac cagccgcctg ccccgcctgc cccgcctgcc       821
325 Ser Ser Thr Ser
326         .   260
328 tgtcccgcca cactggcttt aggacctgtt gacacggagg ggggtttttta atttggtttt  881
330 taacaactca ggggtttgtt tttattttta tttaattttt gcagctcaac ttttaaacaa  941
332 actgcagggg agagggtggg gctggaagga aggctgaggc ctggtcagca gtgaccccag  1001
334 cagagcaggc cccagtcctc ctgggaggct ggcccccctt ttttctgggc cctactgccc  1061
336 tcctctgccc aggaaatggg ggggtttcag caactcagtg tcacagaata aaatcaagtg  1121
338 tggagtgcca taaaaaaaa                                               1140
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342 <211> LENGTH: 260
343 <212> TYPE: PRT
344 <213> ORGANISM: Homo sapiens
346 <400> SEQUENCE: 4
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353             20                  25                  30
356 Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn Met Ala Leu
357         35                  40                  45
360 Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr
361     50                  55                  60
364 Ala Leu Asn Val Pro Leu Tyr Thr His Phe Thr Ser Pro Ile Arg Arg
365 65                  70                  75                  80
368 Phe Ala Asp Val Leu Val His Arg Leu Leu Ala Ala Ala Leu Gly Tyr
369             85                  90                  95
372 Arg Glu Arg Leu Asp Met Ala Pro Asp Thr Leu Gln Lys Gln Ala Asp
373             100                 105                 110
376 His Cys Asn Asp Arg Arg Met Ala Ser Lys Arg Val Gln Glu Leu Ser
377         115                 120                 125
380 Thr Ser Leu Phe Phe Ala Val Leu Val Lys Glu Ser Gly Pro Leu Glu
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384 Ser Glu Ala Met Val Met Gly Ile Leu Lys Gln Ala Phe Asp Val Leu
385 145                 150                 155                 160
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VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: US/09/647,377   TIME: 15:05:40

Input Set : **N:\COPIES\ES.txt**
Output Set: **N:\CRF3\11142001\I647377.raw**

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:19665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:19685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:19689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23